

SEQUENCE LISTING

<110> KRINGLE PHARMA CO., LTD.

<110> Nakamura, Toshikazu

5

<120> Prophylactic and therapeutic agents for asthma

<130> K12F1248

10 <160> 6

<210> 1

<211> 728

<212> PRT

15 <213> Homo sapiens

<400> 1

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu

1 5 10 15

20 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln

20 25 30

Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr

35 40 45

Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val

25 50 55 60

Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr rg Asn Lys Gly Leu

2/12

	65		70		75		80									
	Pro	Phe	Thr	Cys	Lys	Ala	Phe	Val	Phe	Asp	Lys	Ala	Arg	Lys	Gln	Cys
				85					90					95		
	Leu	Trp	Phe	Pro	Phe	Asn	Ser	Met	Ser	Ser	Gly	Val	Lys	Lys	Glu	Phe
5			100					105						110		
	Gly	His	Glu	Phe	Asp	Leu	Tyr	Glu	Asn	Lys	Asp	Tyr	Ile	Arg	Asn	Cys
			115					120						125		
	Ile	Ile	Gly	Lys	Gly	Arg	Ser	Tyr	Lys	Gly	Thr	Val	Ser	Ile	Thr	Lys
			130					135						140		
10	Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	Ser	Ser	Met	Ile	Pro	His	Glu	His
			145					150					155			160
	Ser	Phe	Leu	Pro	Ser	Ser	Tyr	Arg	Gly	Lys	Asp	Leu	Gln	Glu	Asn	Tyr
				165							170				175	
	Cys	Arg	Asn	Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	Phe	Thr	Ser
15			180								185				190	
	Asn	Pro	Glu	Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	Cys	Ser	Glu
			195								200				205	
	Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	Met	Asp
			210								215				220	
20	His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	Thr	Pro
			225								230				235	
	His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	Phe	Asp
				245										250		255
	Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	Cys	Tyr
25			260											265		270
	Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	Thr	Cys

3/12

	275		280		285	
	Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu					
	290		295		300	
	Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile					
5	305		310		315	320
	Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu					
		325		330		335
	His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn					
		340		345		350
10	Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr					
		355		360		365
	Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp					
		370		375		380
	Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met					
15	385		390		395	400
	Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp					
		405		410		415
	Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala					
		420		425		430
20	Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His					
		435		440		445
	Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys					
		450		455		460
	Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu					
25	465		470		475	480
	Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val					

4/12

	485	490	495	
	Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg			
	500	505	510	
	Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp			
5	515	520	525	
	Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr			
	530	535	540	
	Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys			
	545	550	555	560
10	Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly			
	565	570	575	
	Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp			
	580	585	590	
	Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu			
15	595	600	605	
	Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn			
	610	615	620	
	Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu			
	625	630	635	640
20	Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu			
	645	650	655	
	Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp			
	660	665	670	
	Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu			
25	675	685	685	
	Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly			

5/12

690 695 700
 Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
 705 710 715 720
 Leu Thr Tyr Lys Val Pro Gln Ser
 5 725

 <210> 2
 <211> 723
 <212> PRT
 10 <213> Homo sapiens

 <400> 2
 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
 1 5 10 15
 15 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
 20 25 30
 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
 35 40 45
 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
 20 50 55 60
 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
 65 70 75 95
 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
 80 85 90
 25 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
 100 105 110

6/12

Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
 115 120 125
 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
 130 135 140
 5 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
 145 150 155 160
 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg
 165 170 175
 Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg
 10 180 185 190
 Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr
 195 200 205
 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly
 210 215 220
 15 Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe
 225 230 235 240
 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg
 245 250 255
 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His
 20 260 265 270
 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met
 275 280 285
 Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln
 290 295 300
 25 Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro
 305 310 315 320

Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro

335

350

365

380

400

415

430

445

460

480

495

510

525

8/12

Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly
 530 535 540
 Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu
 545 550 555 560
 5 Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu
 565 570 575
 Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile
 580 585 590
 Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser
 10 595 600 605
 Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu
 610 615 620
 Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His
 625 630 635 640
 15 His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala
 645 650 655
 Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu
 660 665 670
 Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro
 20 675 685 685
 Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val
 690 695 700
 Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val
 705 710 715 720
 25 Pro Gln Ser

<210> 3

<211> 2187

<212> DNA

5 <213> Homo sapiens

<400> 3

atgtgggiga ccaaactcct gccagccctg ctgctgcagc atgtccctcct gcctctcctc 60
 ctgctcccca tcgccatccc ctatgcagag ggacaaagga aaagaagaaa tacaattcat 120
 gaattcaaaa aatcagcaaa gactacccta atcaaaatag atccagcact gaagataaaa 180
 10 accaaaaaag tgaatactgc agaccaatgi gctaatagat gtactaggaa taaaggactt 240
 ccattcactt gcaaggcttt tgtttttgat aaagcaagaa aacaatgcct ctggttcccc 300
 ttcaatagca tgtcaagtgg agtgaaaaaa gaatttggcc atgaatttga cctctatgaa 360
 aacaaagact acattagaaa ctgcatcatt ggtaaaggac gcagctacaa gggaacagta 420
 tctatcacta agagtggcat caaatgtcag ccctggagtt ccatgatacc acacgaacac 480
 15 agctttttgc cticgagcta tcggggtaaa gacctacagg aaaactactg tcgaaatcct 540
 cgaggggaag aagggggacc ctggtgtttc acaagcaatc cagaggtacg ctacgaagtc 600
 tgtgacattc cticagtgtc agaagtigaa tgcattgacct gcaatgggga gagttatcga 660
 ggcttcatgg atcatacaga atcaggcaag atttgcagc gcctgggatca tcagacacca 720
 caccggcaca aattcttggc tgaaagatat cccgacaagg gctttgatga taattattgc 780
 20 cgcaatcccg atggccagcc gaggccatgg tgctatactc ttgacctca caccgcctgg 840
 gagiactgtg caattaaaac atgcgctgac aatactatga atgacactga tgttcctttg 900
 gaaacaactg aatgcatcca aggtcaagga gaaggctaca ggggcactgt caataccatt 960
 tggaatggaa ttccatgtca gcgttgggat tctcagtatc ctacagagca tgacatgact 1020
 cctgaaaatt tcaagtgcga ggacctacga gaaaattact gccgaaatcc agatgggtct 1080
 25 gaatcaccct ggtgttttac cactgatcca aacatccgag ttggctactg ctcccaaatt 1140
 ccaaactgtg atatgtcaca tggacaagat tgttatcgtg ggaatggcaa aaattatatg 1200

10/12

ggcaacttat cccaaacaag aiciggacta acatgttcaa tgitgggacaa gaacatggaa 1260
 gacttacatc gtcataatct cigggaacca gatgcaagta agctgaatga gaattactgc 1320
 cgaaatccag atgatgatgc tcatggaccc tgggtgctaca cgggaaatcc actcatctct 1380
 tgggattatt gccctatttc tcgttgtgaa ggtgatacca cacctacaat agtcaattta 1440
 5 gaccatcccc taatatcttg tgccaaaacg aaacaattgc gagttgtaa tgggattcca 1500
 acacgaacaa acataggatg gatgggttagt ttgagataca gaaataaaca tatctgcgga 1560
 ggatcatiga taaaggagag ttgggttctt actgcacgac agtgtttccc ttctcgagac 1620
 ttgaaagatt atgaagcttg gcttgggaatt catgatgtcc acggaagagg agatgagaaa 1680
 tgcaaacagg ttctcaatgt tcccagctg gtatatggcc ctgaaggatc agatctgggt 1740
 10 ttaatgaagc ttgccaggcc tgctgtcctg gatgattttg ttagtacgat tgatttacct 1800
 aattatggat gcacaattcc tgaaaagacc agttgcagtg ttatggctg gggctacact 1860
 ggattgatca actatgatgg cctattacga gggcacatc tctatataat gggaaatgag 1920
 aaatgcagcc agcatcatcg agggaaggct actctgaatg agctgaaat atgtgctggg 1980
 gctgaaaaga ttggatcagg accatgtgag ggggattatg gtggcccact tgtttgtgag 2040
 15 caacataaaa tgagaatggt tcttgggtgc attgttcctg gtcgtggatg tgccattcca 2100
 aatcgtcctg gtatttttgt ccgagtagca tattatgcaa aatggataca caaattatt 2150
 ttaacatata aggtaccaca gtcatag 2187

<210> 4

20 <211> 2172

<212> DNA

<213> Homo sapiens.

<400> 4

25 atgtgggtga ccaaactcct gccagccctg ctgctgcagc atgtcctcct gcattctctc 60
 ctgctcccca tcgcatccc ctatgcagag ggacaaagga aaagaagaaa tacaattcat 120

gaattcaaaa aatcagcaaa gactacccta atcaaaatag atccagcact gaagataaaa 180
 accaaaaaag tgaatactgc agaccaatgt gctaatagat gtactaggaa taaaggactt 240
 ccattcactt gcaaggcttt tgtttttgat aaagcaagaa aacaatgcct ctgggtcccc 300
 ttcaatagca tgtcaagtgg agtgaaaaaa gaatttggcc atgaattiga cctctatgaa 360
 5 aacaaagact acattagaaa ctgcatcatt ggtaaaggac gcagctacaa gggaacagta 420
 tctatcacta agagtggcat caaatgtcag ccttggagtt ccatgatacc acacgaacac 480
 agctatcggg glaaagacct acaggaanaac tactgtcgaa atcctcgagg ggaagaaggg 540
 ggaccttggg gtttcacaag caatccagag gtacgtacg aagtctgtga cattcctcag 600
 tgttcagaag ttgaatgcat gacctgcaat ggggagagtt atcgaggtct catggatcat 660
 10 acagaatcag gcaagatttg tcagcgctgg gatcatcaga caccacaccg gcacaaattc 720
 ttgcttgaag gatatccga caagggttt gatgataatt attgccgcaa tccgatggc 780
 cagccgaggc catgggtgta tactcttgac cctcacaccc gctgggagta ctgtgcaatt 840
 aaaacatgcg ctgacaatac tatgaatgac actgatgttc ctttggaaac aactgaatgc 900
 atccaaggtc aaggagaagg ctacaggggc actgtcaata ccatttggaa tggaaattcca 960
 15 tgtcagcggtt gggatttcta gtatcctcac gagcatgaca tgactcctga aaatttcaag 1020
 tgcaaggacc tacgagaaaa ttactgccga aatccagatg ggcttgaatc acccttgggt 1080
 ttaccactg atccaaacat ccgagtggc tactgtctcc aaattccaaa ctgtgatatg 1140
 tcacatggac aagattgtta tcgtgggaat ggcaaaaatt ataigggcaa cttatcccaa 1200
 acaagatctg gactaacaatg ttcaatgtgg gacaagaaca tggaagactt acatcgicat 1260
 20 atcttctggg aaccagatgc aagtaagctg aatgagaatt actgccgaaa tccagatgat 1320
 gatgctcatg gaccttgggt ctacacggga aatccactca ttcttggga ttattgccct 1380
 atttctcggt gigaagggtg taccacacct acaatagtca atttagacca tcccgttaata 1440
 tcttgtgcca aaacgaaaca atigcgagtt gtaaattggga ttccaacacg aacaaacata 1500
 ggatggatgg ttagtttgag atacagaaat aaacatatct gcggaggatc attgataaag 1560
 25 gagagtggg ttcttactgc acgacagtgt ttcccttctc gagacttgaa agattatgaa 1620
 gcttggcttg gaattcatga tgtccacgga agaggagatg agaaatgcaa acaggttctc 1680

12/12

aatgtttccc agctgggtata tggccctgaa ggatcagatc tggttttaat gaagcttgcc 1740
aggcctgctg tcctggatga ttttggttagt acgattgatt tacctaatta tggatgcaca 1800
attcctgaaa agaccagtig cagtgtttat ggctggggct acactggatt gatcaactat 1860
gatggcctat tacgagtggc acatctctat ataatgggaa atgagaaatg cagccagcat 1920
5 catcgaggga aggtgactct gaatgagtct gaaatatgtg ctggggctga aaagattgga 1980
tcaggaccat gtgaggggga ttatggtggc ccacttgitt gtgagcaaca taaaatgaga 2040
atggttcttg gtgtcattgt tcctggctgt ggatgtgcca ttccaaatcg tcctggtatt 2100
tttgtccgag tagcatatta tgcaaaatgg atacacaaaa ttattttaac atataaggta 2160
ccacagtcac ag 2172

10

<210> 5

<211>

<212> Artificial sequence

<213>

15

<400> 5

cccgtccagc ggtacacatgt gggtgacc 28

<210> 6

20 <211>

<212> Artificial sequence

<213>

<400> 6

25 tacgggatgg actagttaga ctattgtag 29